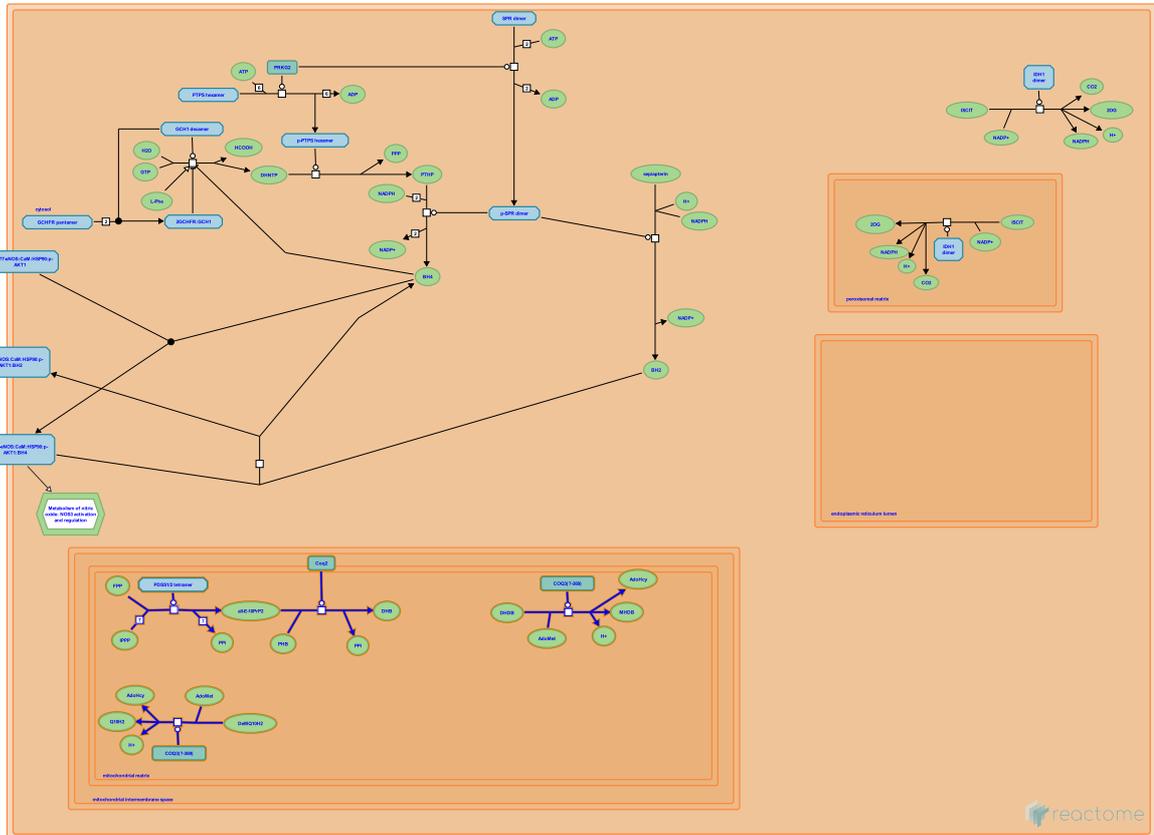# Ubiquinol biosynthesis

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

This is just an excerpt of a full-length report for this pathway. To access the complete report, please download it at the Reactome Textbook.

06/10/2022

Introduction

Reactome is open-source, open access, manually curated and peer-reviewed pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial staff and cross-referenced to many bioinformatics databases. A system of evidence tracking ensures that all assertions are backed up by the primary literature. Reactome is used by clinicians, geneticists, genomics researchers, and molecular biologists to interpret the results of high-throughput experimental studies, by bioinformaticians seeking to develop novel algorithms for mining knowledge from genomic studies, and by systems biologists building predictive models of normal and disease variant pathways.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

Literature references

Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics, 18*, 142. ↗

Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

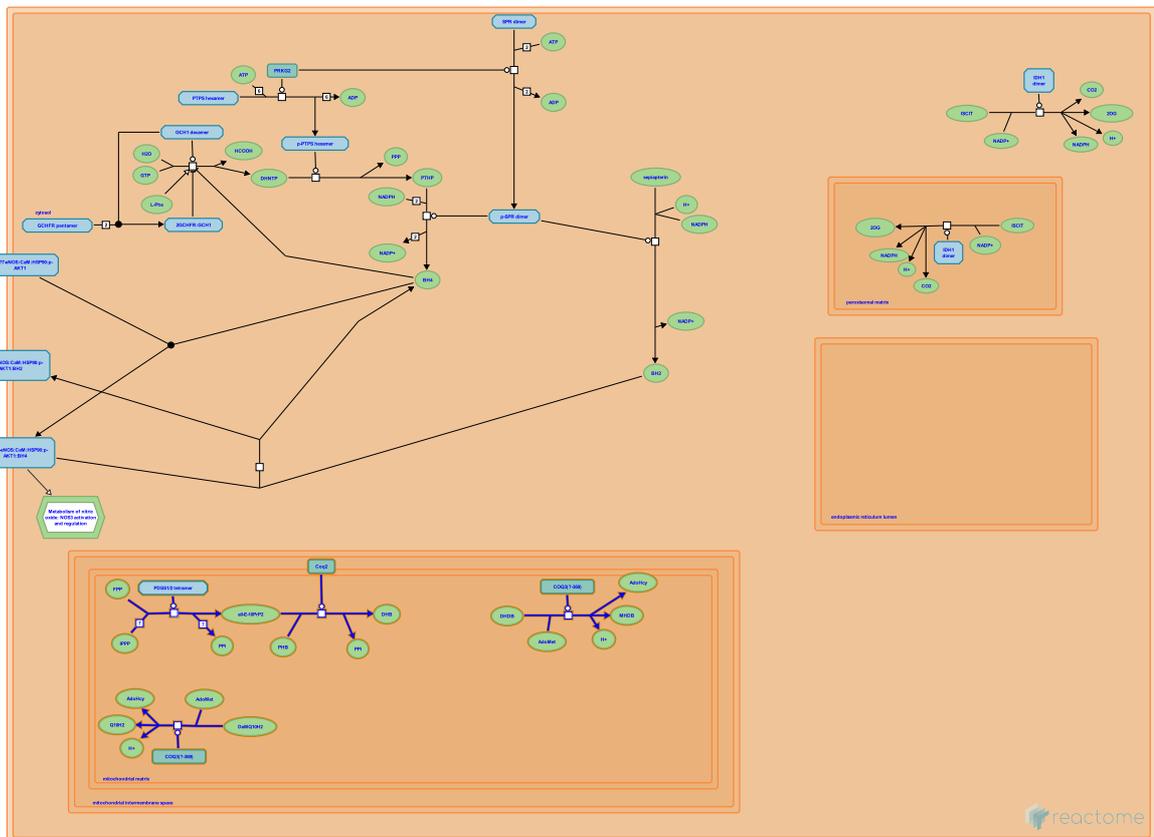Reactome database release: 82

This document contains 1 pathway and 4 reactions (see Table of Contents)

Ubiquinol biosynthesis ↗

Stable identifier: R-MMU-2142789

Inferred from: Ubiquinol biosynthesis (Homo sapiens)

This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

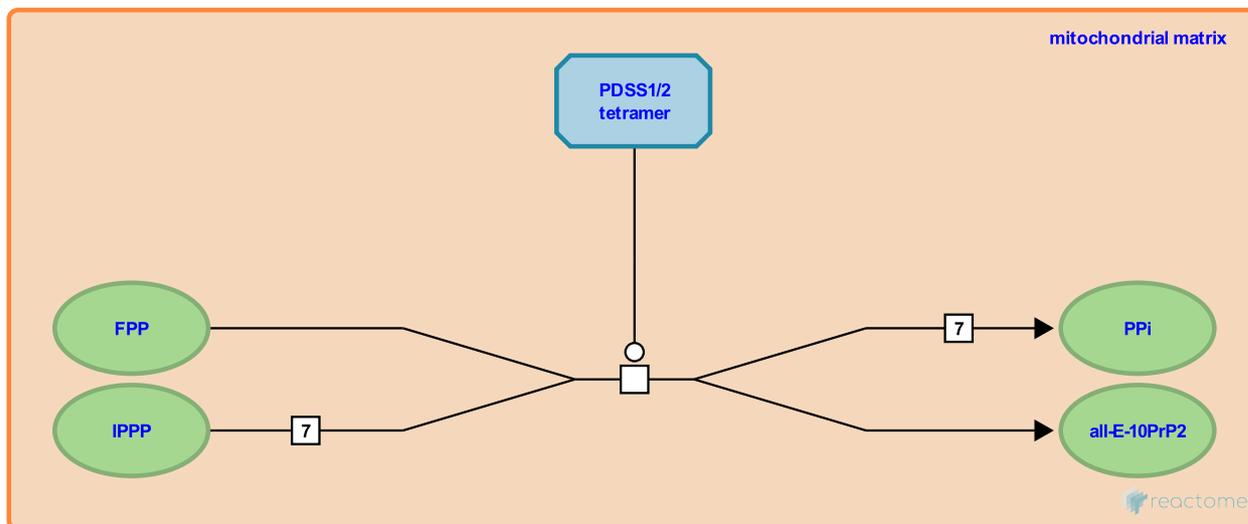## FPP and IPPP are combined into all-E-10PrP2 by PDSS1/2 tetramer ↗

Location: Ubiquinol biosynthesis

Stable identifier: R-MMU-2162253

Type: transition

Compartments: mitochondrial matrix

Inferred from: FPP and IPPP are combined into all-E-10PrP2 by PDSS1/2 tetramer (Homo sapiens)

This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Followed by: PHB and all-E-10PrP2 are combined into DHB by COQ2

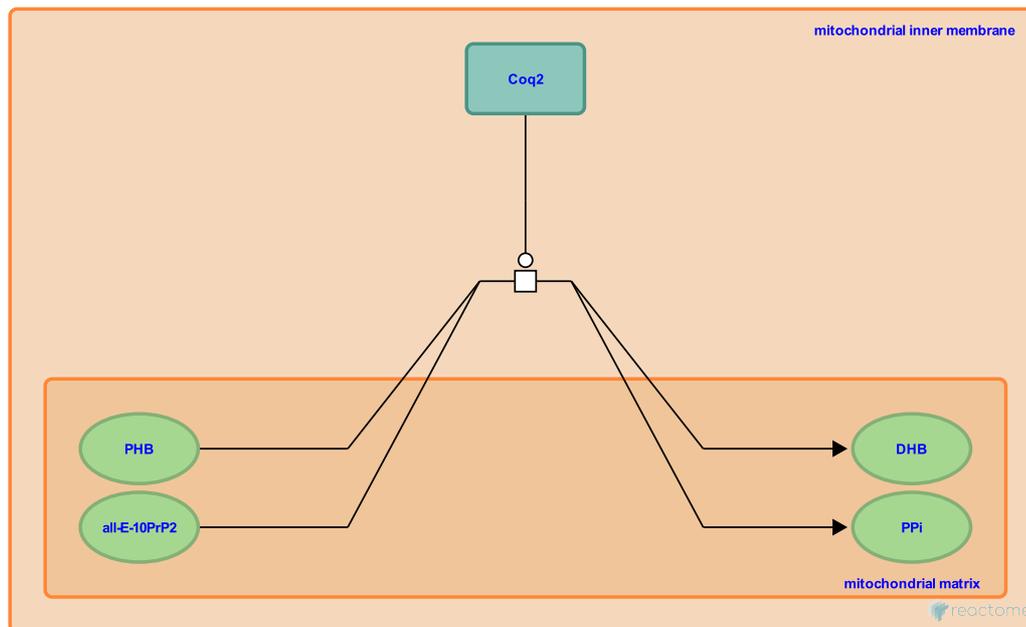## PHB and all-E-10PrP2 are combined into DHB by COQ2 ↗

Location: Ubiquinol biosynthesis

Stable identifier: R-MMU-2162192

Type: transition

Compartments: mitochondrial inner membrane, mitochondrial matrix

Inferred from: PHB and all-E-10PrP2 are combined into DHB by COQ2 (Homo sapiens)

This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Preceded by: FPP and IPPP are combined into all-E-10PrP2 by PDSS1/2 tetramer

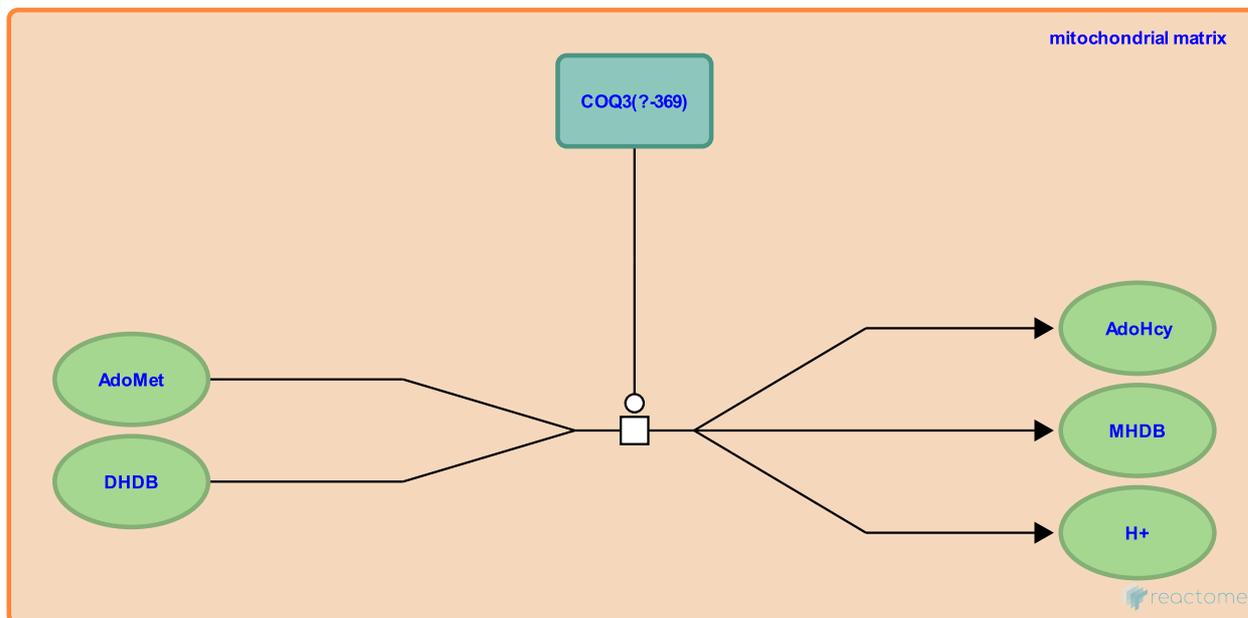# DHDB is methylated to MHDB by COQ3 ↗

Location: Ubiquinol biosynthesis

Stable identifier: R-MMU-2162193

Type: transition

Compartments: mitochondrial matrix

Inferred from: DHDB is methylated to MHDB by COQ3 (Homo sapiens)

This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

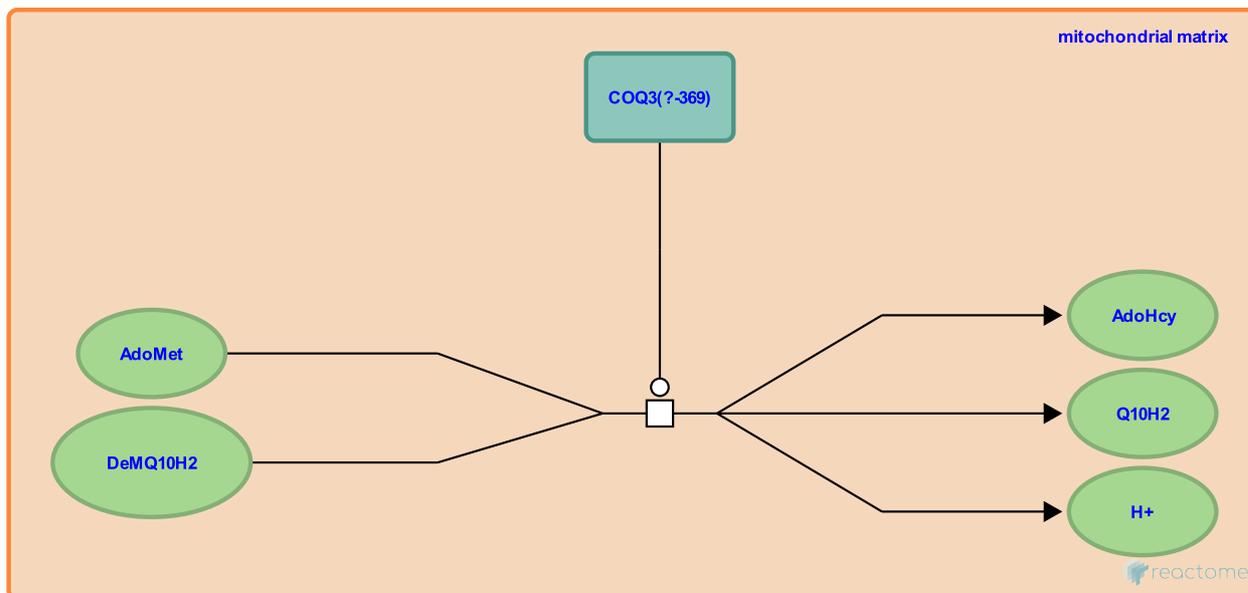# DeMQ10H2 is methylated to Q10H2 by COQ3 ↗

Location: Ubiquinol biosynthesis

Stable identifier: R-MMU-2162186

Type: transition

Compartments: mitochondrial matrix

Inferred from: DeMQ10H2 is methylated to Q10H2 by COQ3 (Homo sapiens)

This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Table of Contents